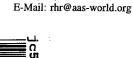
RINES AND RINES ATTORNEYS AT LAW

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April 6, 1999

Commissioner of Patents and Trademarks U S Patent and Trademark Office Washington, DC 20231

Dear Sir

New US Patent Application Entitled: BRCA1 AND hMLHI GENE PRIMER RE. SEQUENCES AND METHOD FOR TESTING

Inventor Jan Vijg, of San Antonio, Texas Corresponding to Provisional Application U.S. Serial No. 60/084408, May 6, 1998

We enclose the above-identified patent application, together with 2 (two) sheets of drawings, and a Verified Statement (small entity status). Declaration (Power of Attorney) will follow shortly

The Commissioner is hereby authorized to charge the filing fee and any additional fees that may be due, to the deposit account No. 18-1425 of the undersigned attorney,

Cordially,

RINES AND RINES

RHR/ipo--Enclosures

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. Applicant or Patentee: Jar	ı Vijg	Attorney's
Serial or Patent No.: Corres Filed or Issued: No. 60/08440	sponding to Provisional US A	application Docket No.:
Filed or Issued: No. 60/08440	Jo, May 0, 1990	To Hook 100
For: BRCA1 and hMLHI Gene Pr	Tiller Sequences that rooms	or rescuing
VERIFIED STA	TEMENT (DECLARATION) CLAIM	ING SMALL ENTITY
	R 1.9(f) and 1.27(b)) - INI	
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As a below named inventor, I as defined in 37 CFR 1.9(c) and (b) of Title 35, United regard to the invention enti	for purposes of paying red States Code, to the Patent	lify as an independent inventor uced fees under section 41(a) and Trademark Office with
described in		
11 the specification	filed berewith 60/084408	_
[v] application serial	DO (Descriptional)	filed May 6 1998
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all statements made on information that these statements were returned like so made are punished of Title 18 of the United Statements.	conation and belief are belined with the knowledge that able by fine or imprisonmentates Code, and that such with application, any patent	own knowledge are true and that eved to be true; and further at willful false statements and at, or both, under section 1001 willful false statements may a issuing thereon, or any patent
<u>Jan Vijg</u>		
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May 6, 1999		•
Date	Date	Date

BRCAI AND hMLHI GENE PRIMER SEQUENCES AND METHOD FOR TESTING

The present application is based upon provisional application 60/084408, filed May 6, 1998, and is directed to methods of and primer sequences for sequence variation and/or mutation detection of BRCA and hMLH1 genes, such as by two-dimensional denaturing gradient electrophoresis techniques (TDGS).

Background

Such techniques are described in Method Of And Apparatus For
Diagnostic DNA Testing, Jan Vijg and Daizong Li, PCT/IB96/00543, filed
3 June 1996, International Publication Number WO96/39535, 12 December 1996,
and in "Two-Dimensional DNA Typing", Molecular Bio Technology, Vol. 4, 1995,
pp 275-295

The tests leading to the establishment of the primer sequences for the BRCAI and hMLH1 of the present invention were conducted with the TDGS design prepared with the computer programming and equipment described in PCT/IB97/00976, published on or about February 14, 1998.

Objects of Invention and Summary

The objects of the invention are to provide novel theoretically and empirically (experimentally) derived TDGS patterns for hMLH1 and BRCA1 genes which may be used by testers to test for gene sequence variation and/or mutations.

Drawings

Figs. 1A and 1B show the computer-aided design TDGS patterns obtained for the hMLH1 and BRCA1 (theoretical-left hand side, empirical or experimental--right hand side)

In the theoretical vs. empirical patterns of the MLHI and BRCA1 genes, for all four genes, one or more exons were designed in overlapping fragments, in which case the fragment name is exon.1, exon..2, etc. Exons 8 and 15 of hMLH1 contain polymorphisms, which can be distinguished from disease-causing heterozygous mutations on the basis of a unique four-spot pattern (18).

Description Of The Invention In Preferred Forms

The MLH1 DNA mismatch repair gene. The design for MLH1 took 30 minutes (excluding exon indication). Fig. 1A shows the theoretical and the empirical TDGS pattern for the MLH1 gene. Because exons 11 and 12 had to be subdivided into overlapping fragments, two multiplex groups are currently being used, with the long PCR carried out as a four-plex PCR. Like many other genes, exon 1 of MLH1 is GC-rich and, hence, was found to melt at a much higher % UF compared to most of the other fragments. Thus far, a total of 41 coded samples with previously identified mutations have been analyzed in a blinded fashion with 100% concordance (30).

The breast and ovarian cancer susceptibility gene BRCA1. The tumor suppressor gene BRCA1 contains 24 exons, of which exon 11 contains approximately 60 % of the coding region. Fig. 1B shows the theoretical and empirical 2-D pattern for BRCA1. Of all 2-D designs discussed, this was the most difficult (total design time was 2 h), the main reason being the need to make overlapping fragments for the 3.4 kb exon 11. Preamplification was accomplished by one 7-plex long PCR. Using the long PCR amplicons as template, all 24 exons were amplified in a total of 37 fragments distributed over 5 multiplex groups. The overlap and sometimes short distances from fragment to fragment necessitated the use of so many multiplex short PCR groups. The non-coding exons 1a, 1b and the non-coding part of exon 24 were excluded. Evaluation of this test design using a panel of coded samples with previously identified mutations is currently ongoing. Thus far, mutations and polymorphisms have been detected in exons 2, 8, 11, 16, 20 and 23.

PCR Amplification

Primers were obtained from Genosys Biotechnologies, Inc. (The Woodlands, TX). For complete lists of all sequences, except BRCA1, see references 18, 29 and 30. Primer sequences for BRCAI will be published elsewhere but will be made available upon request. PCR amplification of gene sequences was carried out using the two-step protocol first described by Li and Vijg (22). Primers for long-distance PCR were designed based on published sequences (24-27) using Primer Designer 3, to amplify the entire genecoding region for each of the 4 genes as a 1-plex (TP53), a 6-plex PCR (RBI), a 4-plex PCR (MLHI) or a 7-plex PCR (BRCAI). The LA PCR kit (Takara) was used for long PCR in a PTC-100 thermocycler (MJ Research). Multiplex short PCR was carried out using the long PCR products as template. Between 0.1 and 1.125 µM of each primer was used in a 50 µl reaction with 1 µl of long PCR product in 20 mM Tris-HCl (pH 8.4), 50 mM KCl, 250 µM of each dNTP and 5 % formamide. Two and a half units of Taq DNA polymerase (Life Technologies) were added after an initial denaturation at 94 °C for 60 s. Cycling conditions for multiplex short PCR and concentrations of MgCl_varied among different genes and amplifications were carried out in a PTC-100 thermocycler (MJ Research).

Two-dimensional DNA electrophoresis

For RB1, 5 µl of multiplex short PCR was used per electrophoresis run. For TP53, MLH1 and BRCA1, 5 µl of each of the different multiplex groups were combined. One tenth of a

volume of loading buffer (0.25 % xviene cvano). 0.25 % bromophenol blue, 15 % ficoll and 100 mM Na,EDTA) was added and the mixtures were loaded onto a 6.5 % (TP53) or 10 % (RB1. MLH1 and BRCA1) PAA non-denaturing size gel (acrylamide: bisacrylamide = 37.5:1) in 0.5 x TAE buffer. The samples were electrophoresed for 5.3 h at 150 V (RB1), 5 h at 120 V (TP53) or 7.5 h at 140 V (MLH1 and BRCA1) at 50 °C. After staining the gel with a mixture of equal amounts of SYBR-green I and II (Molecular Probes, Eugene, Oregon) for 20 min, the region containing all fragments of interest (usually between 100 and 600 bp) was cut out and loaded onto a denaturing gradient gel (DGGE). Gradients used were 0 to 50 % UF for RB1, 20 to 70 % UF for TP53, 25 to 70 % UF for MLH1 and 20 to 65% UF for BRCA1. The second orthogonal dimension was run for 12 h at 100V (RB1), 14 h at 120 V (TP53) or 16 h at 100 V (MLH1 and BRCA1). Spot patterns were visualized by SYBR-green staining using a FluorImager (Molecular Dynamics, Sunnyvale, California).

What is claimed is:

- 1. A method of enabling BRCA1 and h MLHI gene testing for gene sequence variation and/or mutations, that comprises, preparing appropriate test kit primers and solvents suitable for amplifying by long distance PCR the entire gene-coding region of each of BRCA1 and MLHI genes, to be followed by multiplex short PCR using the long PCR products as templates, providing in such test kit appropriate buffer and gel and solvent materials for use in electrophoresis in orthogonal dimensions for producing spot patterns indicative of gene sequence variations and/or mutations.
- 2. The method of claim 1 wherein the test kit is provided with non-denaturing gel and buffer materials suitable to enable combined mixtures of the multiplex groups of BRCA1 and MLHI to be subjected to the electrophoresis simultaneously together.
- 3. The method of claims wherein, the kits provide the Primer Pairs A and B listed in the specification for Long Distance and Short PCR, respectively.
- 4. Test kits for enabling BRCA1 and h MLHI gene testing prepared by the method of claim 3.

ABSTRACT

Primer sequences and materials are pre-prepared as test kits for enabling appropriate gene scanning patterns, preferably by two dimensional electrophoresis (TDGS), for use in detecting sequence variations and/or mutations in BRCA1 and h MLH1 genes

6 The primer sequences for long and short PCR for the BRCA1 are as

follows:

A. Primer Pairs for Long Distance PCR

Exons 1-4

MLH1-4F GCG.GCT.AAG.CTA.CAG.CTG.AAG.GAA.GAA.CGT.GA

MLH1-4R GGC.GAG.ACA.GGA.TTA.CTC.TGA.GAC.CTA.GGC.CC

product size= 10.8kb

Exons 5-10 -

MLH5-10F

GCG.CCC.CTT.GGG.ATT.AGT.ATC.TAT.CTC.TCT.ACT.GG

MLH5-10R GCG.CTC.ATC.TCT.TTC.AAA.GAG.GAG.AGC.CTG

product size=10.5kb

Exons 11-13

MLH11-13F CGG.CTT.TTT.CTC.CCC.CTC.CCA.CTA.TCT.AAG.G

MLH11-13R GGG.TTA.GTA.AAG.GAA.GAG.GAG.CTT.GCC.C

product size=8.7kb

Exons 14-19

MLH14-19F GGT.GCT.TTG.GTC.AAT.GAA.GTG.GGG.TTG.GTA.G

MLH14-19R

GCG.CGC.GTA.TGT.TGG.TAC.ACT.TTG.TAT.ATC.ACA.C

product size=10.5kb

Underlined nucleotides represent nucleotides added to modify melting temperatures of the primers

B. Primer Pairs for Short PCR

Exon Clamp 1 Product Size Tm2 Primer Sequence

12.1	40	184	44.53	TTT.TTT.TTT.TAA.TAC.A
		;		AAT.CTG.TAC.GAA.CCA.TCT
12.2	8	366	53.23	TGG.AAG.TAG.TGA.TAA.GGT
	40			TGT.ACT.TTT.CCC.AAA.AGG
13	40	272	49.06	ATC.TGC.ACT.TCC.TTT.TCT
				AAA.ACC.TTG.GCA.GTT.GAG
14	45	235	48.94	TAC.TTA.CCT.GTT.TTT.TGG
	5			GTA.GTA.GCT.CTG.CTT.GTT
15	40	179	29.97	CAG.CTT.TTC.CTT.AAA.GTC
				CAG.TTG.AAA.TGT.CAG.AAG
16		261	47.56	CTT.GCT.CCT.TCA.TGT.TCT.TG
	40			AGA.AGT.ATA.AGA.ATG.GCT.GTC
17	40	199	47.01	ATT, ATT. TCT. TGT. TCC. CTT
				AAT.GCT.TAG.TAT.CTG.CCT
18	45	215	46.67	CCT.ATT.TTG.AGG.TAT.TGA.AT
				GCC.AGT.GTG.CAT.CAC.CA
19.1		282	43.43	TGT.TGG.GAT.GCA.AAC.AGG
	40			ATC,CCA.CAG.TGC.ATA.AAT

¹GC clamps:

50 clamp:

CGC.CCG.CCG.CCC.GCC.GCC.CGC.GCC.CGC.GC

45 GC clamp:

CGC.CCG.CCG.CCC.GCG.CCC.GTC.CCG.CCC.CCG.CCC.GG

40 clamp:

CGC.CCG.CCG.CCC.GCG.CCC.GGC.CCG.CCG.CCC.CCG.CCC.G

8 clamp:

CGT.CCC.GC

5 clamp:

GCG.CG

2 clamp:

CG

2Tm is given in %UF

The primer sequences for long and short PCR for the BRCA1 are as

follows:

Primers for long-PCR BRCA1 (7-PLEX)

BR1/1-3F

: TgT ACC TTg ATT TCg TAT TCT gAg Agg CTg CTg CTT Ag

BR1/1-3R

: gAg AAA gAA TgA AAT ggA gTT ggA TTT TCg TTC TCA C

Size:

9.9 kb

BR1/5-9F

: TAg CCA TgA AAA gAT AAT CTC ACA ACT gCC CTT AAg AgC

BR1/5-9R

: ACC AgC CTA CTT gAg ggA ggA Agg Tgg gAA gA

Size:

9.7 kb

BR1/10-11F

: gAg AgC AgC TTT CAC TAA CTA AAT AAg ATT ggT CAg CTT

TCT 2T

BRI/10-11R : TCA AgT TTA AgA AgC AgT TCC TTT AAC TAT ACT Tgg AAA

TTT gT

Size:

4.8 kb

BR1/12-13F : gCT Agg ACg TCA TCT TTg gCT TgA ATg AgC TTT A

BR1/12-13R : gCg ATA ATT ACC CAT gTg CTg AgC AAg gAT CA

Size:

9.0 kb

BR1/14-17F : TCT TCA ATg Tgg Agg CAg TAg ggA Tgg AgA AA

BR1/14-17R : ggg TCT CCA ggT TTT gCC TCA CTT gTT CTT TC

Size:

10.7 kb

BR1/18-20F

: TCT TAA CTT CAT ATC AgC CTC CCC TAg ACT TCC AAA TAT

BR1/18-20R : CAT CTC TgC AAA ggg gAg Tgg AAT ACA gAg Tg

Size:

7.2 kb

BR1/21-24F : CAC TCT TCC ATC CCA ACC ACA TAA ATA AgT ATT gTC TC

BR1/21-24R : gCA TAg CCA gAA gTC CTT TTC Agg CTg ATg TAC AT

Size:

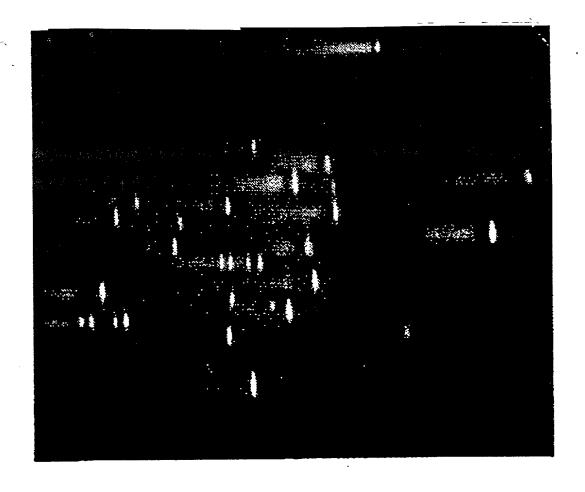
11.4 kb

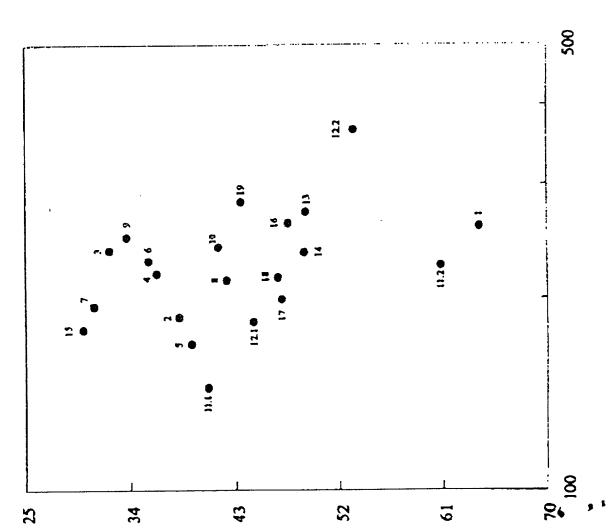
	BClex	11 .		
	Exon	Frag Primers 5' -> 3'	size	Tm (%UF)
		[GC 3] ACCTTGTTATTTTTGTATATTT 22	347	40.99
		[GC 13]TTGCTAAGCCAGGCTGTT 18	-	
		toe 19111001121dcoplocatair 10		
	41.0	[AA 3] AMAAMAANAA AAAAAAA	467	40 24
	11.2	[GC 3]ATACTCATGCCAGCTCATTA 20	461	40.74
		[GC 12] AACGTCCAATACATCAGCTA 20		
	11.3	CATGCTCAGAGAATCCTAGA 20	438	35.04
		[GC 3] CTGTGGCTCAGTAACAAATG 20		
	11 4	[GC 12]TCACTCCAAATCAGTAGAGA 20	476	34.85
		[GC 3]TACTCCTGCTTATAGGTTCA 20	4,0	34.03
		(GC 3) INCIGCIGCTIATAGGITCA 20		
		(mg 4) 0) 1) 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		
	11.5	[GC 3] GAAAGCAGATTTGGCAGTTC 20	468	33.66
		(GC 11) CTGACTGGCATTTGGTTGTA 20		
	11.6	[GC 3]GAATAGGCTGAGGAGGAAGT 20	410	40.51
		[GC 13] CTCTTGGAAGGCTAGGATTG 20		
	11 2	[GC 3] ACAGCGATACTTTCCCAGAG 20	345	36.45
	11.		343	30.45
1		TGCCTTCCCTAGAGTGCTAA 20		
the green speces areas once and the first of				
1.1	11.8	TTGCAAACTGAAAGATCTGT 20	365	38.37
: The		[GC 3]GCTTTGAAACCTTGAATGTA 20		
	11.9	[GC 13]GTCGGGAAACAAGCATAGAA 20	422	10.40
i.i		[GC 4]TTGCCTCTGAACTGAGATGA 20		10,,,0
3 . 3		for all local council desiration and		
trans	11 10	[00 10] TARRAGA GEORGE GEORGE A.		
		[GC 12] TAATATCACTGCAGGCTTTC 20	292	35.93
8;		[GC 1]TTCCTCAAAGTTTTCCTCTA 20		
1 279	11,11	[GC 1] TCCCATCAAGTCATTTGTTA 20	390	33.06
127		TTCCAGGAAGACTTTGTTTA 20		
This field is said that	11.12	[GC 12] TAATGAAGTGGGCTCCAGTA 20	200	33.22
17			309	33.22
1		[GC 1] CTTCCCATAGGCTGTTCTAA 20		
18.3				
	11.13	[GC 1]GCAAGAATATGAAGAAGTAG 20	305	37.43
		CAAATGTGTATGGGTGAAAG 20		
	11.14	[GC 1] AGACACCTGATGACCTGTTA 20	378	43.03
		[GC 12] TCTCCTCTGTGTTCTTAGAC 20	2.0	
		1-1-1-1-10040101041011ROOM 20		
		0000000 44001 01 01 01 01 01 01		
	11.15	CCTTTCACCCATACACATTT 20	460	39.33
	Į	[GC 8] GACTGATGCCTCATTGTTT 20		
	11.16	[GC 3] CTCAGGAACATCACCTTAGT 20	356	44.00
		GC 16)ATAAATAGACTGGGCCACAC 20		
	-			

		AONE n Frag Primers 5' -> 3'	size	Tm(%UF)
	2	1 [GC 1]TATATATGTTTTCTAATGTGT 22 [GC 12]TCCCAAATTAATACACTCTT 20	203	34.64
	3	1 [GC 12] GAGCCTCATTTATTTTCT 18 [GC 4] ATTTTTCGTTCTCACTTA 18	269	37.22
	5	1 [GC 4] TATTTGCCTTTTGAGTAT 18 (GC 12] TCTGATGAATGGTTTTAT 18	305	26.69
	6	1 [GC 8]ACTTGCTGAGTGTGTTTC 18 GCACTTGAGTTGCATTCT 18	213	35.52
	7	1 [GC 3]TACATTTTCTCTAACTGC 19 GAAGAAAACAAATGGTTIT 19	250	32.67
	8	1 GGAGGAAAAGCACAGAAC 18 [GC 3]CCAGCAATTATTATTAAATACTT 23	248	40.51
	9	1 [GC 3] CAGTAGATGCTCAGTAAA 18 AATACCAGCTTCATAGAC 18	242	24.26
	10	1 [GC 4] CTGCATACATGTAACTAG 18 CTACCCACTCTCTTTCA 18	229	38.30
The feet from their	12	1 [GC 4]AGTTGCAGCGTTTATAGT 18 [GC 13]CAGCAAACCTAAGAATGT 18	289	48.54
White the test the first	13	1 [GC 4]GCTTCTCANAGTATTTCA 18 AGTGTTTGGCCAACAATA 18	293	45.18
	14	1 [GC 4] CCAATTTGTGTATCATAG 18 [GC 13] AGTGTATAAATGCCTGTA 18	417	30.78
	15	1 [GC 1]TGGTTTTCTCCTTCCATTTA 20 [GC 16]TGTTCCAATACAGCAGATGA 20	303	46.07
	16	1 [GC 13]CGTTGTGTAAATTAAACTTC 20 [GC 1]AGTCATTAGGGAGATACATA 20	427	47.49
	17	1 [GC 4]TGTGCTAGAGGTAACTCA 18 [GC 11]CTCATGTGGTTTTATGCA 18	242	32.51
	18	1 [GC 12]TTTCAACTTCTAATCCTTT 19 [GC 4]GGAGAAATAGTATTATACT 19	194	36.32
	19	1 GTTCTTCTGCTGTATGTA 18 [GC 4]CTGAATGAATATCTCTGG 18	178	32.32
	20	1 [GC 4]CTCTTCTCTTATCCTGAT 19 TGGTGGGGTGAGATTTTT 18	219	46.40
	21	1 [GC 8] ATTCCCCTGTCCCTCTCT 18	172	49.95

CTGGAACTCTGGGGTTCT 18

1 [GC 4] TGATTTTACATCTAAATGTC 20 [GC 13] AGGAGAGAATATTGTGTC 18	209 47.71
1 [GC 12] TAGTCCTACTTTGACACT 18 [GC 4] AAATATTTAAAATGTGCCAA 20	275 49.47
] [GC 13] AATCTCTGCTTGTGTTCTCT 20	325 59.79





BRCA1

